

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Nelson, Edward L.
Nelson, Peter J.
- (ii) TITLE OF INVENTION: NOVEL VECTOR FOR
POLYNUCLEOTIDE VACCINES
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 - (B) STREET: 345 PARK AVENUE
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: USA
 - (F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US97/14306
 - (B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US60/023931
 - (B) FILING DATE: 14-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: KATHRYN M. BROWN
 - (B) REGISTRATION NUMBER: 34556
 - (C) REFERENCE/DOCKET NUMBER: 2026-4236US1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 758-4800
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 - (C) TELEX: 421792

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:1:

GGCCGCGTTG	CTGGCGTTTT	TCCATAGGCT	CCGCCCCCCT	40
GACGAGCATC	ACAAAAATCG	ACGCTCAAGT	CAGAGGTGGC	80
GAAACCCGAC	AGGACTATAA	AGATACCAGG	CGTTTCCCCC	120
TGGAAGCTCC	CTCGTGCGCT	CTCCTGTTCC	GACCCTGCCG	160
CTTACCGGAT	ACCTCTCCGC	CTTTCTCCCT	TCGGGAAGCG	200
TGGCGCTTTC	TCAATGCTCA	CGCTGTAGGT	ATCTCAGTTC	240
GGTGTAGGTC	GTTCGCTCCA	AGCTGGGCTG	TGTGCACGAA	280
CCCCCGTTTC	AGCCCGACCG	CTGCGCCTTA	TCCGGTAACT	320
ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATCGCC	360
ACTGGCAGCA	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	400
TATGTAGGCG	GTGCTACAGA	GTTCTTGAAG	TGGTGGCCTA	440
ACTACGGCTA	CAC			453

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:2:

GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	AACTCTGTAG	40
CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCACT	80
GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	TACCGGGTTG	120
GAICTAAGAC	GATAGTTACC	GGATAAGGCG	CAGCGGTCGG	160
GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA	GCTTGGAGCG	200
AACGACCTAC	ACCGAACTGA	GATACCTACA	CCGTGAGCAT	240
TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	AAGGCGGACA	280
GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	GAGAGCGCAC	320
GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	TCTTTATAGT	360
CCTGTCGGGT	TTCGCCACCT	CTGACTTGAG	CGTCGATTTT	400
TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	GGAAAAACGC	440
CAGCAACGCG	GCC			453

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:3:

GAATTCTTTC	GGACTTTTGA	AAGTGATGGT	GGTGGCCGAA	40
GGATTCTGAAC	CTTCGAAGTC	GATGACGGCA	GATTTAGAGT	80
CTGCTCCCTT	TGGCCGCTCG	GGAACCCAC	CACGGGTAAT	120
GCTTTTACTG	GCCTGCTCCC	TTATCGGGAA	GCGGGGCGCA	160
TCATATCAAA	TGACGCGCCG	CTGTAAAGTG	TTACGTTGAG	200
AAAGAATTC				209

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:4:

GAATTCTTTC	TCAACGTAAAC	ACTTTACAGC	GGCGCGTCAT	40
TTGATATGAT	GCGCCCCGCT	TCCCGATAAG	GGAGCAGGCC	80
AGTAAAAGCA	TTACCCGTGG	TGGGGTTCCC	GAGCGGCCAA	120
AGGGAGCAGA	CTCTAAATCT	GCCGTCATCG	ACTTCGAAGG	160
TTCGAATCCT	TCCCCACCA	CCATCACTTT	CAAAAGTCCG	200
AAAGAATTC				209

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:5:

AATAAA

6

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:6:

ATTAAA

6

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:7:

AGTAAA

6

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:8:

AAGAAC

6

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

AATACA

6

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:10:

GCCTTAAGGG	CCATATGGTG	AGTGGATCCC	TTGACCCCAG	40
GCGGGGATGG	GGAGACCTGT	AGTCAGAGCC	CCCGGGCAGC	80
ACAGGCCAAT	GCCCCGTCCTT	CCCCTGCAGG	ATGAGTAGTG	120
AGTGCCCTCTC	CTGGCCCTGG	AAGTTGCCAC	TCCAGTGCCC	160
ACCAGCCTTG	TCCTAATAAA	ATTAAGTTGC	ATCATTTTGT	200
CTGACTAGGT	GTCCTCTATA	ATATTAT		227

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:11:

ATAATATTAT	AGAGGACACC	TAGTCAGAAC	AAATGATGCA	40
ACTTAATTTT	ATTAGGACAA	GGCTGGTGGG	CACTGGAGTG	80
GCAACTTCCA	GGGCCAGGAG	AGGCACTCAC	TACTCATCCT	120
GCAGGGGAAG	GACGGGCATT	GGCCTGTGCT	GCCCGGGGGC	160
TCTGACTACA	GGTCTCCCCC	ATCCCCGCCT	GGGGTCAAGG	200
CATCCACTCA	CCATATGGCC	CTTAAGG		227

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:12:

CCTCGGTACC	TGCCATGGCG	CGGATTCTTT	ATCACTGATA	40
AGTTGGTGGA	CATATTATGT	TTATCAGTGA	TAAAGTGTCA	80
AGCATGACAA	AGTTGCAGCC	GAATACAGTG	ATCCGTGCCG	120
GCCCTGGACT	GTTGAACGAG	GTCGGCGTAG	ACGGTCTGAC	160
GACACGCAAA	CTGGCGGAAC	GGTTGGGGGT	GCAGCAGCCG	200
GCGCTTTACT	GGCACTTCAG	GAACAAGCGG	GCGCCTTAAG	240
GGCCATATGC	CG			252

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

CCTCGGTACC TGCCACCATG GCGCGGATTC TTTAT

35

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:14:

CGGCATATGG CCTTAAGGCG CCCGCTTGTT CCTGAAGT

38

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:15:

GCCTTAAGGG CCATATGGTG AGTGGATGCC TTGACCCCGAG
GCGGGGATGG GGGAGACCTG TAGTCAGAGC CCCCAGGCAG

40
80

CACAGGCCAA TGCCCGTCCT TCCCCTGCAG GATGAGTAGT
GAGTGCCTCT CCTGGCCCTG GAAGTTGCCA CTCCAGTGCC
CACCAGCCTT GTCCTAATAA AATTAAGTTG CATCATTTTG
TCTGACTAGG TGTCCTCTAT AATATTAT

120
160
200
228

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:16:

TGCCATGGCG	CGGATTCTTT	ATCACTGATA	AGTTGGTGGA	40
CATATTATGT	TTATCAGTGA	TAAAGTGTCA	AGCATGACAA	80
AGTTGCAGCC	GAATACAGTG	ATCCGTGCCG	GCCCTGGACT	120
GTTGAACGAG	GTCGGCGTAG	ACGGTCTGAC	GACACGCAAA	160
CTGGCGGAAC	GGTTGGGGGT	GCAGCAGCCG	GCGCTTTACT	200
GGCACTTCAG	GAACAAGCGG	GCGCCTTAAG	GGCCATATGG	240
TGAGTGGAATG	CCTTGACCCC	AGGCGGGGAT	GGGGGAGACC	280
TGTAGTCAGA	GCCCCCGGGC	AGCACAGGCC	AATGCCCCGTC	320
CTTCCCCTGC	AGTGAGTAGT	GACTGCCCGG	GTGGGATCCC	360
TGTGACCCCT	CCCCAGTGCC	TCTCCTGGCC	CTGGAAGTTG	400
CCACTCCAGT	GCCCACCAGC	CTTGTCCTAA	TAAAATTAAG	440
TTGCATCATT	TTGTCTGACT	AGGTGTCCTC	TATAATATTA	480
TAAGCTTGAT	ATCGAATTCT	TTCTCAACGT	AACACTTTAC	520
AGCGGCGCGT	CATTTGATAT	GATGCGCCCC	GCTTCCCGAT	560
AAGGGAGCAG	GCCAGTAAAA	GCATTACCCG	TGGTGGGGTT	600
CCCGAGCGGC	CAAAGGGAGC	AGACTCTAAA	CTGCCGTCA	640
TCGACTTCGA	AGGTTCTGAAT	CCTTCCCCCA	CCACCATCAC	680
TTTCAAAAGT	CCGAAAGAAT	TCCTGCAGCC	CGTGTAGCCG	720
TAGTTAGGCC	ACCACTTCAA	GAACCTCTGT	GCACCGCCTA	760
CATACCTCGC	TCTGCTAATC	CTGTTACCAG	TGGCTGCTGC	800
CAGTGGCGAT	AAGTCGTGTC	TTACCGGGTT	GGACTCAAGA	840
CGATAGTTAC	CGGATAAGGC	GCAGCGGTCG	GGCTGAACGG	880
GGGGTTCTGT	CACACAGCCC	AGCTTGGAGC	GAACGACCTA	920
CACCGAACTG	AGATACCTAC	AGCGTGAGCA	TTGAGAAAGC	960
GCCACGCTTC	CCGAAGGGAG	AAAGGCGGAC	AGGTATCCGG	1000
TAAGCGGCAG	GGTCGGAACA	GGAGAGCGCA	CGAGGGAGCT	1040
TCCAGGGGGA	AACGCCTGGT	ATCTTTATAG	TCCTGTCGGG	1080
TTTCGCCACC	TCTGACTTGA	GCGTCGATTT	TTGTGATGCT	1120
CGTCAGGGGG	GCGGAGCCTA	TGGAAAAACG	CCAGCAACGC	1160
GGCCGGGGGA	TCCGGAGAGC	TCACTCTAGA	TGAGAGAGCA	1200
GTGAGGGAGA	GACAGAGACT	CGAATTTCCG	GAGCTATTTT	1240
AGTTTTCTTT	TCCGTTTTGT	GCAATTTTAC	TTATGATACC	1280
GGCCAATGCT	TGGTTGCTAT	TTTGGAAGCT	CCCCTTAGGG	1320
GATGCCCTTC	AACTGGCCCT	ATAAAGGGCC	AGCCTGAGCT	1360
GCAGAGGATT	CCTGCAGAGG	ATCAAGACAG	CACGTGGACC	1400
TCGCACAGCC	TCTCCACAG	GTACC		1425

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:17:

ATGAGCAAGG	GCGAGGAACT	GTTCACTGGC	GTGGTCCCAA	40
TTCTCGTGGA	ACTGGATGGC	GATGTGAATG	GGCACAAATT	80
TTCTGTCAGC	GGAGAGGGTG	AAGGTGATGC	CACATACGGA	120
AAGCTCACCC	TGAAATTTCAT	CTGCACCACT	GGAAAGCTCC	160
CTGTGCCATG	GCCAACACTG	GTCACTACCT	TCACCTATGG	200
CGTGCAAGTG	TTTTCCAGAT	ACCCAGACCA	TATGAACGAG	240
CATGACTTTT	TCAAGAGCGC	CATGCCCGAG	GGCTATGTGC	280
AGGAGAGAAC	CATCTTTTTC	AAAGATGACG	GGAACACTAA	320
GACCCGCGCT	GAAGTCAAGT	TCGAAGGTGA	CACCCTGGTG	360
AATAGAATCG	AGTTGAAGGG	CATTGACTTT	AAGGAAGATG	400
GAAACATTCT	CGGCCACAAG	CTGGAATACA	ACTATAACTC	440
CCACAATGTG	TACATCATGG	CCGACAAGCA	AAAGAATGGC	480
ATCAAGGTCA	ACTTCAAGAT	CAGACACAAC	ATTGAGGATG	520
GATCCGTGCA	GCTGGCCGAC	CATTATCAAC	AGAACACTCC	560
AATCGGCGAC	CGCCCTGTGC	TCCTCCCAGA	CAACAATTAC	600
CTGTCCACCC	AGTCTGCCCT	GTCTAAAGAT	CCCAACGAAA	640
AGAGAGACCA	CATGGTCCTG	CTGGAGTTTG	TGACCGCTGC	680
TGGGATCACA	CATGGCATGG	ACGAGCTGTA	CAAGTGAGC	719

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:18:

0924200-109

TATGAGCAAG	GGCGAGGAAC	TGTTCACTGG	CGTGGTCCCA	40
ATTCTCGTGG	AACTGGATGG	CGATGTGAAT	GGGCACAAAT	80
TTTCTGTGAG	CGGAGAGGGT	GAAGGTGATG	CCACATACGG	120
AAAGCTCACC	CTGAAATTCA	TCTGCACCAC	TGGAAAGCTC	160
CCTGTGCCAT	GGCCAACACT	GGTCACTACC	TTCACCTATG	200
GCGTGCACTG	CTTTTCCAGA	TACCCAGACC	ATATGAAGCA	240
GCATGACTTT	TTCAAGAGCG	CCATGCCCCG	GGGCTATGTG	280
CAGGAGAGAA	CCATCTTTTT	CAAAGATGAC	GGGAACCTACA	320
AGACCCGCGC	TGAAGTCAAG	TTCGAAGGTG	ACACCCCTGGT	360
GAATAGAATC	GAGTTGAAGG	GCATTGACTT	TAAGGAAGAT	400
GGAAACATTC	TCGGCCACAA	GCTGGAATAC	AACTATAACT	440
CCCACAATGT	GTACATCATG	GCCGACAAGC	AAAAGAATGG	480
CATCAAGGTC	AACTTCAAGA	TCAGACACAA	CATTGAGGAT	520
GGATCCGTGC	AGCTGGCCGA	CCATTATCAA	CAGAACACTC	560
CAATCGGCCG	CGGCCCTGTG	CTCCTCCCAG	ACAACCATTA	600
CCTGTCCACC	CAGTCTGCCC	GTCTAAAGAT	CCCAACGAAA	640
AGAGAGACCA	CATGGTCTCT	CTGGAGTTTG	TGACCGCTGC	680
TGGGATCACA	CATGGCATGG	ACGAGCTGTA	CAAGTGAGCC	720
ATATGGTGAG	TGGATGCCTT	GACCCCAGGC	GGGGATGGGG	760
GAGACCTGTA	GTCAGAGCCC	CCGGGCAGCA	CAGGCCAATG	800
CCCGTCCTTC	CCCTGCAGTG	AGTAGTGACT	GCCCAGGTGG	840
GATCCCTGTG	ACCCCTCCCC	AGTGCCCTCT	CTGGCCCTGG	880
AAGTTGCCAC	TCCAGTGCCC	ACCAGCCTTG	TCCTAATAAA	920
ATTAAGTTGC	ATCATTTTGT	CTGACTAGGT	GTCTCTCTATA	960
ATATTATAAG	CTTGATATCG	AATTCTTTCT	CAACGTAACA	1000
CTTTACAGCG	GCGCGTCATT	TGATATGATG	CGCCCCGCTT	1040
CCCGATAAGG	GAGCAGGCCA	GTAAGAGCAT	TACCCGTGGT	1080
GGGGTTCCCG	AGCGGCCAAA	GGGAGCAGAC	TCTAAATCTG	1120
CCGTCAATCG	CTTCGAAGGT	TCGAATCCTT	CCCCACCAC	1160
CATCACTTTC	AAAAGTCCGA	AAGAATTCTT	GCAGCCCGTG	1200
TAGCCGTAGT	TAGGCCACCA	CTTCAAGAAC	TCTGTAGCAC	1240
CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCAGTGGC	1280
TGCTGCCAGT	GGCGATAAGT	CGTGTCTTAC	CGGGTTGGAC	1320
TCAAGACGAT	AGTTACCGGA	TAAGGCGCAG	CGGTCGGGCT	1360
GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC	1400
GACCTACACC	GAAGTGAAGT	ACCTACAGCG	TGAGCATTGA	1440
GAAAGCGCCA	CGCTTCCCGA	AGGGAGAAAG	GCGGACAGGT	1480
ATCCGGTAAG	CGGCAGGGTC	GGAACAGGAG	AGCGCACGAG	1520
GGAGCTTCCA	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	1560
GTCGGGTTTC	GCCACCTCTG	ACTTGAGCGT	CGATTTTTGT	1600
GATGCTCGTC	AGGGGGGCGG	AGCCTATGGA	AAAACGCCAG	1640
CAACGCGGCC	GGGGGATCCG	GAGAGCTCAC	TCTAGATGAG	1680
AGAGCAGTGA	GGGAGAGACA	GAGACTCGAA	TTTCCGGAGC	1720
TATTTCAAGT	TTCTTTTCCG	TTTTGTGCAA	TTTCACTTAT	1760
GATACCGGCC	AATGCTTGGT	TGCTATTTTG	GAAACTCCCC	1800
TTAGGGGATG	CCCCCTCACT	GGCCCTATAA	AGGGCCAGCC	1840
TGAGCTGCAG	AGGATTCCTG	CAGAGGATCA	AGACAGCACG	1880
TGGACCTCGC	ACAGCCTCTC	CCACAGGTAC	C	1911

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:19:

```

Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro
 1          5          10
Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn
          15          20
Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly
25          30          35
Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser
          40          45
Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
50          55          60
Val Leu Gly Val Val Phe Gly Ile Leu
          65
  
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:20:

```

Pro Ala Pro Gly Ala Gly Gly Met Val His His Arg
 1          5          10
His Arg Ser Ser Ser Thr Arg Ser Gly Gly Gly Asp
          15          20
Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala
25          30          35
Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly
          40          45
Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala
50          55          60
Ala Lys Gly Leu Ser Leu Pro Thr His Asp Pro Ser
          65          70
Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro
75          80
Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu
85          90          95

Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
          100          105
Asp Val Arg Pro Pro Pro Ser Pro Arg Glu Gly Pro
110          115          120

Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
          125          130
Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val
135          140
  
```

Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu
 145 150 155
 Asn Pro Glu Tyr Leu Thr Pro Gln Gly Thr Cys Ser
 160 165
 Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg
 170 175 180
 Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
 185 190
 Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro
 195 200
 Lys Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
 205 210 215
 Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu
 220 225
 Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro
 230 235 240
 His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn
 245 250
 Leu Tyr Tyr Trp Asp Asp Pro Pro Glu Arg Gly Ala
 255 260
 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu
 260 270 275
 Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Val
 280 285

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:21:

Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
 1 5 10
 Val Leu Gly Val Val Phe Gly Ile Leu Ile
 15 20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:22:

GCCACCATGG	CCCCTGACCT	CTCCTACATG	CCCATCTGGA	40
AGTTTCCAGA	TGAGGAGGGC	GCATGCCAGC	CTTGCCCCAT	80
CAACTGCACC	CACTCCTGTG	TGGACCTGGA	TGACAAGGGC	120
TGCCCCGCCG	AGCAGAGAGC	CAGCCCTCTG	ACGTCCATCA	160
TCTCTGCGGT	GGTTGGCATT	CTGCTGGTCG	TGGTCTTGGG	200
GGTGGTCTTT	GGGATCCTCA	TCAAGCGACG	GCAGCAGAAG	240
ATCACATGTC	CAGACCCTGC	CCCGGGCGCT	GGGGGCATGG	280
TCCACCACAG	GCACCGCAGC	TCATCTACCA	GGAGTGGCGG	320
TGGGGACCTG	ACACTAGGGC	TGGAGCCCTC	TGAAGAGGAG	360
GCCCCCAGGT	CTCCACTGGC	ACCCTCCGAA	GGGGCTGGCT	400
CCGATGTATT	TGATGGTGAC	CTGGGAATGG	GGGCAGCCAA	440
GGGGCTGCAA	AGCCTCCCCA	CACATGACCC	CAGCCCTCTA	480
CAGCGGTACA	GTGAGGACCC	CACAGTACCC	CTGCCCTCTG	520
AGACTGATGG	CTACGTTGCC	CCCCTGACCT	GCAGCCCCCA	560
GCCTGAATAT	GTGAACCAGC	CAGATGTTTC	GCCCCAGCCC	600
CCTTCGCCCC	GAGAGGGCCC	TCTGCCTGCT	GCCCCGACCTG	640
CTGGTGCCAC	TCTGGAAAGG	CCCAAGACTC	TCTCCCCAGG	680
GAAGAATGGG	GTCGTCAAAG	ACGTTTTTTC	CTTTGGGGGT	720
GCCGTGGAGA	ACCCCGAGAC	TTGACACCCC	AGGGAGGAGC	760
TGCCCCCTCAG	CCCCACCTTC	CTCCTGCCTT	CAGCCCAGCC	800
TTCGACAACC	TCTATTACTG	GGACCAGGAC	CCACCAGAGC	840
GGGGGGCTCC	ACCCAGCACC	TTCAAAGGGA	CACCTACGGC	880
AGAGAACCCA	GAGTACCTGG	GTCTGGACGT	GCCAGTGTGA	920
AGCCTTAAGG	GCCATATGGT	GAGTGGATGC	CTTGACCCCCA	960
GGCGGGGATG	GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	1000
GCACAGGCCA	ATGCCCCGTC	TTCCCCTGCA	GTGAGTAGTG	1040
ACTGCCCCGG	TGGGATCCCT	GTGACCCCTC	CCCAGTGCCT	1080
CTCCTGGCCC	TGGAAGTTGC	CACTCCAGTG	CCCACCAGCC	1120
TTGTCTCTAAT	AAAATTAAGT	TGCATCATTT	TGTCTGACTA	1160
GGTGTCTCT	ATAATATTAT	AAGCTTGATA	TCGAATTCTT	1200
TCTCAACGTA	ACACTTTACA	GCGGCGCGTC	ATTTGATATG	1240
ATGCGCCCCG	CTTCCCGATA	AGGGAGCAGG	CCAGTAAAGG	1280
CATTACCCGT	GGTGGGGTTC	CCGAGCGGCC	AAAGGGAGCA	1320
GACTCTAAAT	CTGCCGTCAT	CGACTTCGAA	GGTTCGAATC	1360
CTTCCCCCAC	CACCATCACT	TTCAAAAGTC	CGAAAGAATT	1400
CCTGCAGCCC	GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	1440
AACTCTGTAG	CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	1480
TGTTACCAGT	GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	1520
TACCGGGTTG	GACTCAAGAC	GATAGTTACC	GGATAAGGCG	1560
CAGCGGTCGG	GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA	1600
GCTTGAGAGC	AACGACCTAC	ACCGAACTGA	GATACCTACA	1640
GCGTGAGCAT	TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	1680
AAGGCGGACA	GGTATCCGGT	AAGCGGCAGG	GTCCGGAACAG	1720
GAGAGCGCAC	GAGGGAGCTT	CCAGGGGAA	ACGCCTGGTA	1760
TCTTTATAGT	CCTGTCGGGT	TTCCGCCACCT	CTGACTTGAG	1800
CGTCGATTTT	TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	1840
GGAAAAACGC	CAGCAACGCG	GCCGGGGGAT	CCGGAGAGCT	1880
CACTCTAGAT	GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	1920
GAATTTCCGG	AGCTATTTCA	GTTTTCTTTT	CCGTTTTGTG	1960

CAATTTCACT	TATGATACCG	GCCAATGCTT	GGTTGCTATT	2000
TTGGAAACTC	CCCTTAGGGG	ATGCCCTCA	ACTGGCCCTA	2040
TAAAGGGCCA	GCCTGAGCTG	CAGAGGATTC	CTGCAGAGGA	2080
TCAAGACAGC	ACGTGGACCT	CGCACAGCCT	CTCCCACAGG	2120
TACCT				2125

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:23:

GTCTGCCACC ATGGCCTACT CCCCTGC

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:24:

TTCTTTGGTG ACCTACCTCT TCGGAATTGC CGAGTC

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(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: No
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:25:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC 40
TGAGTCAGGA AACATTTTCA GACCTATGGA AACTACTTCC 80
TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG 120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT 160
TCACTGAAGA CCCAGGTCCA GATGAAGCTC CCAGAATGCC 200
AGAGGCTGCT CCCCGCGTGG CCCCTGCACC AGCAGCTCCT 240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT 280
CATCTTCTGT CCCTTCCCAG AAAACCTACC AGGGCAGCTA 320
CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG 360
TCTGCCACCA TGGCCTACTC CCCTGCGTCT GTGACTTGCA 400
CGTACTCCCC TGCCCTCAAC AAGATGTTTT GCCAACTGGC 440
CAAGACCTGC CCTGTGCAGC TGTGGGTTGA TTCCACACCC 480
CCGCCCGGCA CCCGCGTCCG CGCCATGGCC ATCTACAAGC 520
AGTCACAGCA CATGACGGAG GTTGTGAGGC GCTGCCCCCA 560
CCATGAGCGC TGCTCAGATA GCGATGGTCT GGCCCCCTCCT 600
CAGCGTCTTA TCCGAGTGGA AGGAAATTTG CGTGTGGAGT 640
ATTTGGATGA CAGAAACACT TTTCGACATA GTGTGGTGGT 680
GCCCTATGAG CCGCCTGAGG TTGGCTCTGA CTGTACCACC 720
ATCCACTACA ACTACATGTG TAACAGTTCC TGCATGGGCG 760
GCATGAACCG GAGGCCCATC CTCACCATCA TCACACTGGA 800
AGACTCCAGT GGTAATCTAC TGGGACGGAA CAGCTTTGAG 840
GTGCGTGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG 880
AGGAAGAGAA TCTCCGCAAG AAAGGGGAGC CTCACCACGA 920
GCTGCCCCCA GGGAGCACTA AGCGAGCACT GCCCAACAAC 960
ACCAGCTCCT CTCCCCAGCC AAAGAAGAAA CCACTGGATG 1000
GAGAATATTT CACCCTTCAG ATCCGTGGGC GTGAGCGCTT 1040
CGAGATGTTT TTTGGTGACC TACCTCTTCG GAATTGCCGA 1080
GTCTTCCGAG AGCTGAATGA GGCCTTGGA CTCAAGGATG 1120
CCCAGGCTGG GAAGGAGCCA GGGGGGAGCA GGGCTCACTC 1160
CAGCCACCTG AAGTCCAAA AGGGTCAGTC TACCTCCCGC 1200
CATAAAAAAC TCATGTTCAA GACAGAAGGG CCTGACTCAG 1240
AC 1242

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 608 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:26:

CTCGGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	40
CCCTGACGAG	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	80
TGGCGAAACC	CGACAGGACT	ATAAAGATAC	CAGGCGTTTC	120
CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	160
GCCGCTTACC	GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	200
AGCGTGGCGC	TTTCTCAATG	CTCACGCTGT	AGGTATCTCA	240
GTTGCGGTGTA	GGTCGTTTCG	TCCAAGCTGG	GCTGTGTGCA	280
CGAACCCCCC	GTTTCAGCCC	ACCGCTGCGC	CTTATCCGGT	320
AACTATCGTC	TTGAGTCCAA	CCCGGTAAGA	CACGACTTAT	360
CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	400
GAGGTATGTA	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	440
CCTAACTACG	GCTACACTAG	AAGGACAGTA	TTTGGTATCT	480
GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	520
TAGCTCTTGA	TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	560
GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	CGCAGAAAAA	600
AAGGATCT				608

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:27:

GGTACCTGCC	ACCATGGCGC	GGATTCTTTA	TCACTGATAA	40
GTTGGTGGAC	ATATTATGTT	TATCAGTGAT	AAAGTGTCAA	80
GCATGACAAA	GTTGCAGCCG	AATACAGTGA	TCCGTGCCGG	120
CCCTGGACTG	TTGAACGAGG	TCGGCGTAGA	CGGTCTGACG	160
ACACGCAAAC	TGGCGGAACG	GTTGGGGGTG	CAGCAGCCGG	200
CGCTTTACTG	GCACTTCAGG	AACAAGCGGG	CGCCTTAAGG	240
GCCATATGGT	GAGTGGATGC	CTTGACCCCA	GGCGGGGATG	280
GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	GCACAGGCCA	320
ATGCCCGTCC	TTCCCCTGCA	GGATGAGTAG	TGAGTGCCTC	360
TCCTGGCCCT	GGAAGTTGCC	ACTCCAGTGC	CCACCAGCCT	400
TGTCCTAATA	AAATTAAGTT	GCATCATTTT	GTCTGACTAG	440
GTGTCCTCTA	TAATATTATA	AGCTTGATAT	CGAATTCTTT	480
CGGACTTTTG	AAAGTGATGG	TGGTGGGGGA	AGGATTCGAA	520
CCTTCGAAGT	CGATGACGGC	AGATTTAGAG	TCTGCTCCCT	560
TTGGCCGCTC	GGGAACCCCA	CCACGGGTAA	TGCTTTTACT	600
GGCCTGCTCC	CTTATCGGGA	AGCGGGGCGC	ATCATATCAA	640
ATGACGCGCC	GCTGTAAAGT	GTTACGTTGA	GAAAGAATTC	680
CTGCAGCCCC	CCGCGTTGCT	GGCGTTTTTC	CATAGGCTCC	720

GCCCCCTGA	CGAGCATCAC	AAAAATCGAC	GCTCAAGTCA	760
GAGGTGGCGA	AACCCGACAG	GACTATAAAG	ATACCAGGCG	800
TTTCCCCCTG	GAAGCTCCCT	CGTGCGCTCT	CCTGTTCCGA	840
CCCTGCCGCT	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC	880
GGGAAGCGTG	GCGCTTTCTC	AATGCTCACG	CTGTAGGTAT	920
CTCAGTTTCG	TGTAGGTCGT	TCGCTCCAAG	CTGGGCTGTG	960
TGCACGAACC	CCCCGTTTCA	CCCGACCGCT	GCGCCTTATC	1000
CGGTAACAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	1040
TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	1080
GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG	1120
GTGGCCTAAC	TACGGCTACA	CTAGAAGGAC	AGTATTTGGT	1160
ATCTGCGCTC	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG	1200
TTGGTAGCTC	TTGATCCGCG	AAACAAACCA	CCGCTGGTAG	1240
CGGTGGTTTT	TTTGTTTGCA	AGCAGCAGAT	TACGCGCAGA	1280
AAAAAAGGAT	CTGGGGGATC	CGGAGAGCTC	ACTCTAGATG	1320
AGAGAGCAGT	GAGGGAGAGA	CAGAGACTCG	AATTTCCGGA	1360
GCTATTTTCA	TTTTCTTTTC	CGTTTGTGTC	AATTTCACTT	1400
ATGATACCGG	CCAATGCTTG	GTTGCTATTT	TGGAAACTCC	1440
CCTTAGGGGA	TGCCCCCTCA	CTGGCCCTAT	AAAGGGCCAG	1480
CCTGAGCTGC	AGAGGATTCC	TGCAGAGGAT	CAAGACAGCA	1520
CGTGGACCTC	GCACAGCCTC	TCCCACA		1547

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGTACCTGCC	ACCATGGCGC	GGATTCTTTA	TCACTGATAA	40
GTTGGTGGAC	ATATTATGTT	TATCAGTGAT	AAAGTGTCAA	80
GCATGACAAA	GTTGCAGCCG	AATACAGTGA	TCCGTGCCGG	120
CCCTGGACTG	TTGAACGAGG	TCGGCGTAGA	CGGTCTGACG	160
ACACGCAAAC	TGGCGGAACG	GTTGGGGGTG	CAGCAGCCGG	200
CGCTTTACTG	GCACTTCAGG	AACAAGCGGG	CGCCTTAAGG	240
GCCATATGGT	GAGTGGATGC	CTTGACCCCA	GGCGGGGATG	280
GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	GCACAGGCCA	320
ATGCCCCGCC	TTCCCCTGCA	GGATGAGTAG	TGAGTGCCTC	360
TCCTGGCCCT	GGAAGTTGCC	ACTCCAGTGC	CCACCAGCCT	400
TGTCTTAATA	AAATTAAGTT	GCATCATTTT	GTCGTACTAG	440
GTGTCTCTTA	TAATATTATA	AGCTTGATAT	CGAATTCTTT	480
CGGACTTTTG	AAAGTGATGG	TGGTGGGGGA	AGGATTTCGAA	520
CCTTCGAAGT	CGATGACGGC	AGATTTAGAG	TCTGCTCCCT	560
TTGGCCGCTC	GGGAACCCCA	CCACGGGTAA	TGCTTTTACT	600
GGCCTGCTCC	CTTATCGGGA	AGCGGGGCGC	ATCATATCAA	640
ATGACGCGCC	GCTGTAAAGT	GTTACGTTGA	GAAAGAATTTC	680

CTGCAGCCCG	CCGCGTTGCT	GGCGTTTTTC	CATAGGCTCC	720
GCCCCCCTGA	CGAGCATCAC	AAAAATCGAC	GCTCAAGTCA	760
GAGGTGGCGA	AACCCGACAG	GACTATAAAG	ATACCAGGCG	800
TTTCCCCCTG	GAAGCTCCCT	CGTGCGCTCT	CCTGTTCCGA	840
CCCTGCCGCT	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC	880
GGGAAGCGTG	GCGCTTTCTC	AATGCTCACG	CTGTAGGTAT	920
CTCAGTTCGG	TGTAGGTCGT	TCGCTCCAAG	CTGGGCTGTG	960
TGCACGAACC	CCCCGTTTCA	CCCGACCGCT	GCGCCTTATC	1000
CGGTAACAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	1040
TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	1080
GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG	1120
GTGGCCTAAC	TACGGCTACA	CTAGAAGGAC	AGTATTTGGT	1160
ATCTGCGCTC	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG	1200
TTGGTAGCTC	TTGATCCGGC	AAACAAACCA	CCGCTGGTAG	1240
CGGTGGTTTT	TTTGTGTTGCA	AGCAGCAGAT	TACGCGCAGA	1280
AAAAAAGGAT	CTGGGGGATC	CGGAGAGCTC	CCAACGCGTT	1320
GGATGCATGG	ATGAGGGAAA	GGAGGTAAGA	TCTGTAATGA	1360
ATAAGCAGGA	ACTTTGAAGA	CTCAGTGACT	CAGTGAGTAA	1400
TAAAGACTCA	GTGACTTCTG	ATCCTGTCTT	AACTGCCACT	1440
CCTTGTTGTC	CCAAGAAAGC	GGCTTCCTGC	TCTCTGAGGA	1480
GGACCCCTTC	CCTGGAAGGT	AAAATAAGG	ATGTCAGCAG	1520
AGAAATTTTT	CCACCATTTG	TGCTTGGTCA	AAGAGGAAAC	1560
TGATGAGCTC	ACTCTAGATG	AGAGAGCAGT	GAGGGAGAGA	1600
CAGAGACTCG	AATTTCCGGA	GCTATTTTCA	TTTTCTTTTC	1640
CGTTTTGTGC	AATTTCACTT	ATGATACCGG	CCAATGCTTG	1680
GTTGCTATTT	TGGAAACTCC	CCTTAGGGGA	TGCCCTCAA	1720
CTGGCCCTAT	AAAGGGCCAG	CCTGAGCTGC	AGAGGATTCC	1760
TGCAGAGGAT	CAAGACAGCA	CGTGGACCTC	GCACAGCCTC	1800
TCCCCACA				1807

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:29:

GGTACCTGCC	ACCATGGCGA	AGGGCGAGGA	ACTGTTCACT	40
GGCGTGGTCC	CAATTCTCGT	GGAAGTGGAT	GGCGATGTGA	80
ATGGGCACAA	ATTTTCTGTC	AGCGGAGAGG	GTGAAGGTGA	120
TGCCACATAC	GGAAAGCTCA	CCCTGAAATT	CATCTGCACC	160
ACTGGAAAGC	TCCCTGTGCC	ATGGCCAACA	CTGGTCACTA	200
CCTTCACCTA	TGGCGTGCAG	TGCTTTTCCA	GATACCCAGA	240
CCATATGAAG	CAGCATGACT	TTTTCAAGAG	CGCCATGCCC	280

GAGGGCTATG	TGCAGGAGAG	AACCATCTTT	TTCAAAGATG	320
ACGGGAACCTA	CAAGACCCGC	GCTGAAGTCA	AGTTCGAAGG	360
TGACACCCTG	GTGAATAGAA	TCGAGTTGAA	GGGCATTGAC	400
TTTAAGGAAG	ATGGAAACAT	TCTCGGCCAC	AAGCTGGAAT	440
ACAACCTATAA	CTCCCACAAT	GTGTACATCA	TGGCCGACAA	480
GCAAAAGAAT	GGCATCAAGG	TCAACTTCAA	GATCAGACAC	520
AACATTGAGG	ATGGATCCGT	GCAGCTGGCC	GACCATTATC	560
AACAGAACAC	TCCAATCGGC	GACGGCCCTG	TGCTCCTCCC	600
AGACAACCAT	TACCTGTCCA	CCCAGTCTGC	CCTGTCTAAA	640
GATCCCAACG	AAAAGAGAGA	CCACATGGTC	CTGCTGGAGT	680
TTGTGACCGC	TGCTGGGATC	ACACATGGCA	TGGACGAGCT	720
GTACAAGTGA	GCGCCTTAAG	GGCCATATGG	TGAGTGGATG	760
CCTTGACCCC	AGGCGGGGAT	GGGGGAGACC	TGTAGTCAGA	800
GCCCCCGGGC	AGCACAGGCC	AATGCCCCTG	CTTCCCCTGC	840
AGGATGAGTA	GTGAGTGCCT	CTCCTGGCCC	TGGAAGTTGC	880
CACTCCAGTG	CCCACCAGCC	TTGTCCTAAT	AAAATTAAGT	920
TGCATCATTT	TGTCTGACTA	GGTGTCTCT	ATAATATTAT	960
AAGCTTGATA	TCGAATTCTT	TCGGACTTTT	GAAAGTGATG	1000
GTGGTGGGGG	AAGGATTCGA	ACCTTCGAAG	TCAATGACGG	1040
CAGATTTAGA	GTCTGCTCCC	TTTGGCCGCT	CGGGAACCCC	1080
ACCACGGGTA	ATGCTTTTAC	TGGCCTGCTC	CCTTATCGGG	1120
AAGCGGGGCG	CATCATATCA	AATGACGCGC	CGCTGTAAAG	1160
TGTTACGTTG	AGAAAGAATT	CCTGCAGCCC	GCCGCGTTGC	1200
TGGCGTTTTT	CCATAGGCTC	CGCCCCCCTG	ACGAGCATCA	1240
CAAAAATCGA	CGCTCAAGTC	AGAGGTGGCG	AAACCCGACA	1280
GGACTATAAA	GATACCAGGC	GTTTCCCCCT	GGAAGCTCCC	1320
TCGTGCGCTC	TCCTGTTCCG	ACCCTGCCGC	TTACCGGATA	1360
CCTGTCCGCC	TTTCTCCCTT	CGGGAAGCGT	GGCGCTTTCT	1400
CAATGCTCAC	GCTGTAGGTA	TCTCAGTTCG	GTGTAGGTCG	1440
TTCGCTCCAA	GCTGGGCTGT	GTGCACGAAC	CCCCCGTTCA	1480
GCCCCGACCG	TGCGCCTTAT	CCGGTAACCTA	TCGTCTTGAG	1520
TCCAACCCGG	TAAGACACGA	CTTATCGCCA	CTGGCAGCAG	1560
CCACTGGTAA	CAGGATTAGC	AGAGCGAGGT	ATGTAGGCGG	1600
TGCTACAGAG	TTCTTGAAGT	GGTGGCCTAA	CTACGGCTAC	1640
ACTAGAAGGA	CAGTATTGGA	TATCTGCGCT	CTGCTGAAGC	1680
CAGTTACCTT	CGGAAAAAGA	GTTGGTAGCT	CTTGATCCGG	1720
CAAACAAACC	ACCGCTGGTA	GCGGTGGTTT	TTTTGTTTGC	1760
AAGCAGCAGA	TTACGCGCAG	AAAAAAAGGA	TCTGGGGGAT	1800
CCGGAGAGCT	CCCAACGCGT	TGGATGCATG	GATGAGGGAA	1840
AGGAGGTAAG	ATCTGTAATG	AATAAGCAGG	AACTTTGAAG	1880
ACTCAGTGAC	TCAGTGAGTA	ATAAAGACTC	AGTGACTTCT	1920
GATCCTGTCC	TAACTGCCAC	TCCTTGTTGT	CCCAAGAAAG	1960
CGGCTTCCCT	CTCTCTGAGG	AGGACCCCTT	CCCTGGAAGG	2000
TAAAACTAAG	GATGTCAGCA	GAGAAATTTT	TCCACCATTG	2040
GTGCTTGGTC	AAAGAGGAAA	CTGATGAGCT	CACCTCTAGAT	2080
GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	GAATTTCCGG	2120
AGCTATTTCA	GTTTTCTTTT	CCGTTTTGTG	CAATTTCACT	2160
TATGATACCG	GCCAATGCTT	GGTTGCTATT	TTGGAAACTC	2200
CCCTTAGGGG	ATGCCCTTCA	ACTGGCCCTA	TAAAGGGCCA	2240
GCCTGAGCTG	CAGAGGATTC	CTGCAGAGGA	TCAAGACAGC	2280
ACGTGGACCT	CGCACAGCCT	CTCCACA		2308